

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 25.3953 Seconds

(without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613B-11
Perfect score: 577
Sequence: 1 SDMLTFQKHLTNRVDNCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: ELOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_21:
1: sp.archaea:
2: sp.bacteria:
3: sp.fungi:
4: sp.human:
5: sp.invertebrate:
6: sp.mammal:
7: sp.mhc:
8: sp.organelle:
9: sp.phage:
10: sp.plant:
11: sp rodent:
12: sp.virus:
13: sp.vertibrate:
14: sp.unclassified:
15: sp.virus:
16: sp.bacteriap:
17: sp.archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	99.3	127	13	0918V8
2	551	95.5	127	13	08UVX5
3	399.5	69.2	129	13	09DFY6
4	381	66.0	128	13	09DFY8
5	306	53.0	128	13	09DFY7
6	304	52.7	128	13	09DFY5
7	293	50.8	133	13	098SM0
8	287	49.7	133	13	098SM7
9	281	48.7	132	13	098SM2
10	281	48.7	133	13	098SM2
11	277	48.0	133	13	098SL8
12	275	47.7	132	13	098SM1
13	270.5	46.9	132	13	09DF78
14	157.5	27.3	169	13	09W738
15	133	23.1	152	11	09JKT5
16	131	22.7	157	11	09JKT9

17	130.5	22.6	153	11	09JKT7	09JKT7 mus saxicol
18	130	22.5	157	11	09JKT3	09JKT3 meriones un
19	127	22.0	154	11	09JKT8	09JKT8 mus saxicol
20	127	22.0	157	11	09JKT4	09JKT4 meriones un
21	126	21.8	157	11	09JKT1	09JKT1 meriones un
22	125	21.7	157	11	09JKT2	09JKT2 meriones un
23	124.5	21.6	155	11	09JKT9	09JKT9 mus pahari
24	123.5	21.4	155	11	09JKT3	09JKT3 mus saxicol
25	120.5	20.9	155	11	09JKT6	09JKT6 mus saxicol
26	119.5	20.7	155	11	09JKT4	09JKT4 mus saxicol
27	119.5	20.7	155	11	09JKT2	09JKT2 mus saxicol
28	117.5	20.4	155	11	09R134	09R134 ratius norv
29	117	20.3	156	11	09JKT7	09JKT7 mus caroli
30	117	20.3	156	11	09JKT6	09JKT6 mus caroli
31	116.5	20.2	132	6	09RV25	09RV25 enlemur ful
32	116.5	20.2	155	11	09R125	09R125 mus musculu
33	116.5	20.2	155	11	09JKT8	09JKT8 mus pahari
34	116	20.1	155	11	09JKT7	09JKT7 mus caroli
35	115	19.9	156	11	09JKT5	09JKT5 mus caroli
36	115	19.9	156	11	09JKT4	09JKT4 mus caroli
37	115	19.9	156	11	09JKT9	09JKT9 mus caroli
38	114.5	19.8	132	6	09RV24	09RV24 galago mono
39	114.5	19.8	170	6	09BEC1	09BEC1 tiragulus ja
40	113.5	19.7	119	6	09TS06	09TS06 cercopithec
41	113.5	19.7	119	6	09RV32	09RV32 gorilla gor
42	112.5	19.5	119	6	09RV30	09RV30 saguinus oe
43	112	19.4	124	6	09RSF2	09RSF2 bos taurus
44	112	19.4	156	11	09JKT6	09JKT6 mus musculu
45	112	19.4	156	11	09VHS0	09VHS0 mus musculu

ALIGNMENTS

RESULT 1

ID	0918V8	PRELIMINARY;	PRT;	127 AA.
AC	0918V8:			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Onconase variant rapuri precursor.			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=20330357; PubMed=10871370;			
RA	Chen S.-L., Le S.-Y., Newton D.L., Matzel J.V., Jr., Rybak S.M.,			
RT	"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a			
RT	3' UTR of unusual length and structure."			
RL	Nucleic Acids Res. 28:2375-2382(2000).			
DR	EMBL: AF165133; AAF76935.1;			
DR	HSSP: P22069; IONC.			
DR	InterPro: IPR001427; RNaseA.			
DR	Efam: PF00074; RNaseA. 1.			
DR	ProDom: PD000535; RNaseA. 1.			
DR	SMART: SM00092; RNase_Pc. 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
KW	Signal.			
FT	SIGNAL. 1 23			POTENTIAL.
SQ	SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;			

QY	2	DMLTFQKHLTNRVDNCNIMSTNLFHCKDKNTPIYSRPEVYKAICKIISKVNLTT5 61
DB	25	DMLTFQKHLTNRVDNCNIMSTNLFHCKDKNTPIYSRPEVYKAICKIISKVNLTT5 84

QY	62	EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	104
Db	85	EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	127

RESULT 2			
ID	Q8UVX5	PRELIMINARY;	PRT; 127 AA.
AC	Q8UVX5		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
DE	Oncomase precursor.		
GN	RPR.		
OS	Rana pipiens (Northern leopard frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
OX	NCBI_TaxID=8404;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Liao Y.-D., Wang S.-C.;		
RT	"Rana pipiens oncomase genomic DNA";		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF332139; AAI54383.1; -		
DR	InterPro: IPR001427; RNaseA.		
DR	Pfam: PF00074; rnasea; 1.		
DR	ProDom: PD000535; RNaseA; 1.		
DR	SMART: SM00092; RNase_Pc.1.		
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.		
KW	Signal.		
FT	SIGNAL		
SO	SEQUENCE	1 23	POTENTIAL.
		127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;	

Query Match			
Best Local Similarity	95.5%;	Score 551;	DB 13;
Matches	99;	Conservative	2;
		Mismatches	2;
		Indels	0;
		Gaps	0;
QY	2	DMLTQKKHLITRDVDCNNINSTMFLHCKDKNFTIYSRPEFVAKICGIIASKNVLTTS	61
Db	25	DMLTQKKHLITRDVDCNNINSTMFLHCKDKNFTIYSRPEFVAKICGIIASKNVLTTS	84
QY	62	EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	104
Db	85	EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC	127

RESULT 3			
ID	Q9DFY6	PRELIMINARY;	PRT; 129 AA.
AC	Q9DFY6		
DT	01-MAR-2001 (TReMBLrel. 16, Created)		
DT	01-OCT-2001 (TReMBLrel. 18, Last sequence update)		
DT	01-DEC-2001 (TReMBLrel. 19, Last annotation update)		
DE	RC-RNase4 ribonuclease precursor.		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
OX	NCBI_TaxID=8400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIVER.		
RA	MEDLINE=20512555; Pubmed=11058105;		
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;		
RT	"Purification and cloning of cytototoxic ribonucleases from Rana		
RL	catesbeiana (bullfrog)."		
RL	Nucleic Acids Res. 28:4097-4104(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=LIVER.		
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;		
RA	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
RL	EMBL: AF242555; AAG31441.2; -		
RS	HSSP: P22069; IONC.		

DR	InterPro:IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA. 1.	
DR ProDom: PD000535; RNaseA. 1.	
DR SMART: SM00092; RNase_PC. 1.	
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.	
KW Signal.	
FT SIGNAL.	
FT CHAIN	1 23 POTENTIAL.
SQ SEQUENCE	129 AA: 14724 MW: 826A62882B10ABDA CRC64;
Query Match	
Best Local Similarity	69.2%; Score 399.5; DB 13; Length 129;
Matches	70; Conservative 16; Mismatches 17; Indels 1; Gaps 1
OY	2 DWLTFQKKHLTNRDVCNNINMSTNLFHCKDKNTFIYSRPPEVKAICKGIISKNVLTTS 61
DB	25 DWATFEKKHLTPTWDVCDNMPTSLFDCKDNKTFIYSLPGVKALCGRVFSADVLNS 84
OY	62 EFLYSDCNVTSR-PCKYKLKSKTNTEFCVGCNQAVHPFVGHC 104
DB	85 EFLYAECCNKPKRKPCYKLKSKSNRICTRCHELPFHAFVAGVIC 128
RESULT 4	
ID Q9DFY8	PRELIMINARY; PRT: 128 AA.
AC Q9DFY8:	
DT 01-MAR-2001 (TREMBLrel. 16, Created)	
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)	
OS RC-RNase2 ribonuclease precursor.	
OC Rana catesbeiana (Bull frog).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.	
NCBI_Txid=8400;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=LIVER;	
RX MEDLINE=20512555; PubMed=11058105;	
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;	
"Purification and cloning of cytoloxic ribonucleases from Rana	
catesbeiana (bullfrog).";	
RL Nucleic Acids Res. 28:4097-4104(2000).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC TISSUE=LIVER;	
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;	
Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL: AF242553; AAC31439.1;	
DR HSSP: P22069; IONC.	
DR InterPro: IPR001427; RNaseA.	
DR Pfam: PF00074; rnaaseA. 1.	
DR ProDom: PD000535; RNaseA. 1.	
DR SMART: SM00092; RNase_PC. 1.	
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.	
KW Signal.	
FT SIGNAL.	1 23 POTENTIAL.
FT CHAIN	24 128 RC-RNase2 RIBONUCLEASE.
SQ SEQUENCE	128 AA: 14839 MW: 989719CF52053ECC CRC64;
Query Match	
Best Local Similarity	66.0%; Score 381; DB 13; Length 128;
Matches	69; Conservative 10; Mismatches 24; Indels 0; Gaps 0;
OY	2 DWLTFQKKHLTNRDVCNNINMSTNLFHCKDKNTFIYSRPPEVKAICKGIISKNVLTTS 61
DB	25 DWLTFQKKHLTNRDVCNNINMSTNLFHCKDKNTFIYSRPPEVKAICKGIISKNVLTTS 61
OY	62 EFLYSDCNVTSR-PCKYKLKSKTNTEFCVGCNQAVHPFVGHC 104
DB	85 EFLYSDCNVTSR-PCKYKLKSKTNTEFCVGCNQAVHPFVGHC 104

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RESULT 5
O9DFY7 ID 09DFY7 PRELIMINARY: PRT: 128 AA.
AC 09DFY7:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20513555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytototoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL: AF242554; AAG31440.2;
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 12814986082E0587D CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 2.3e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

OY 2 DMLTFQKHILNTRDVCNNIMSTNLFPCCKDNFTFYSRPREPKAICGIIASKNVLTTS 61
DB 25 DMLTFQKHILNTRDVCNNIMSTNLFPCCKDNFTFYSRPREPKAICGIIASKNVLTTS 61
OY 62 EFTLSDCNVTSPCKYKLRKSTNFCVCENQAPVHFEVGHG 104
DB 85 AFLPQCRRKRLPCHYKRLSSSTNFTICLVNQLPIHFAGVSC 127

RESULT 6
O9DFY5 ID 09DFY5 PRELIMINARY: PRT: 128 AA.
AC 09DFY5:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytototoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL: AF242556; AAG31442.2;
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.

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DR Pfam: PF00074; RNaseA; 1.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFBFB67D266C7C2 CRC64;

Query Match 52.7%; Score 304; DB 13; Length 128;
Best Local Similarity 53.4%; Pred. No. 3.8e-27;
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

OY 2 DMLTFQKHILNTRDVCNNIMSTNLFPCCKDNFTFYSRPREPKAICGIIASKNVLTTS 61
DB 25 DMLTFQKHILNTRDVCNNIMSTNLFPCCKDNFTFYSRPREPKAICGIIASKNVLTTS 61
OY 62 EFTLSDCNVTSPCKYKLRKSTNFCVCENQAPVHFEVGHG 104
DB 85 VFYLPQCNRRKRLPCHYRLDGSSTNFTICLVNQLPIHFAGVSC 127

RESULT 7
O9BSMO ID 09BSMO PRELIMINARY: PRT: 133 AA.
AC 09BSMO:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351209; AAK30255.1;
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.8%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 7.2e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 2 DMLTFQKHILNTRDVCNNIMSTNLFPCCKDNFTFYSRPREPKAICGIIASKNV 57
DB 24 DMLTFQKHILNTRDVCNNIMSTNLFPCCKDNFTFYSRPREPKAICGIIASKNV 57
OY 58 LTTSEFYSDC---NVTSPCKYKLRKSTNFCVCENQAPVHFEVGHG 104
DB 83 LSTRFQNLNCTRTSITPRPCYSRTENNYICVGCENQYVHFGIORC 132

RESULT 8
O9PWR7 ID 09PWR7 PRELIMINARY: PRT: 133 AA.
AC 09PWR7:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Ribonuclease precursor.

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GN	RCR.				
OS	Rana catesbeiana (Bull frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_TaxID=8400;				
RM	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=LIVER;				
RX	MEDLINE=96165825; PubMed=9497370;				
RA	Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;				
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.				
RT	Tissue distribution, cloning, purification, cytotoxicity, and active				
RT	residues for RNase activity.";				
RL	J. Biol. Chem. 273:6395-6401(1998).				
DR	EMBL: AF039104; AAD10702.1; --				
DR	HSSP: P11916; IBC4.				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; rnaasea. 1.				
DR	Prodom: PD000535; RNaseA. 1.				
DR	SMART: SM00092; RNase_Pc. 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.				
KW	Signal.				
FT	SIGNAL				
FT	CHAIN	1	22	POTENTIAL.	
FT	CHAIN	23	133	RIBONUCLEASE.	
SQ	SEQUENCE	133 AA;	14762 MW;	A7D62594FFD16F0C	CRC64;

Query Match	49.7%	Score 287	DB 13	Length 133
Best Local Similarity	49.1%	Pred No. 3.5e-25		
Matches 54	Conservative 16	Mismatches 32	Indels 8	Gaps .3

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QY 2 DWLFFQCKHLTNRDVCQNNIMSTNLF---HCKDKNTFLYSPSEPVAKIILSKNV 57
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 NMATFQCKHLTINPIINCNTIMDNIIYVGGQCKRNFIFISATTVKALCTGV-NNMV 82
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 LTTSEFLTSC---NVTSRCKTKKLKSTFTFCVTCENQAPVHFVVGHC 104
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 LSTRFDLNTCTRTSTLRPCPYSSRRENTYVCKENQVPMHFAIGC 132
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 9	
Q98SM2	
ID Q98SM2	PRELIMINARY;
AC Q98SM2	PRT; 132 AA

DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Rnase A-type ribonuclease rc203 precursor (RC-Rnase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
RX NCBI_TaxId=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RT bullfrog, *Rana catesbeiana*.";
RL J. Mol. Evol. 53:31-38(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF351207; AKK30253.1; -
DR EMBL; AF359578; AAL87036.1; -
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW signal.
FT SIGNAL. 1 22 POTENTIAL.

FT	CHAIN	23	132	RC-RNASE7.
SQ	SEQUENCE	132 AA;	14412 MN;	131A745187978687 CRC64

Query Match	48.7%	Score 281	DB 13	Length 132
Best Local Similarity	47.7%	Pred. No. 1.7e-24		
Matches	52	Conservative	14	Mismatches 35
				Indels 8
				Gaps 3

[illegible]

RESULT 10	
Q98SL9	
ID Q98SL9	PRELIMINARY;
008810	PRT; 133 AA

DT	01-JUN-2001 (TREMblrel. 17, Created)
DT	01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT	01-DEC-2001 (TREMblrel. 19, last annotation update)
DE	Rnase A-type ribonuclease rc212 precursor.
OS	Rana catesbeiana (bull frog).
OC	Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Embryophyta; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OX	NCBI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21539506; PubMed=11683320;
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT	"Rapid diversification of Rnase A superfamily ribonuclease from the
RL	bullfrog, Rana catesbeiana.";
J	Mol. Evol. 53:31-38(2001).
EMBL	AF351210; AAC30256.1; -.
HSSP	P11916; IBC4.
InterPro	IPR001427; RNaseA.
Pfam	PF000074; rnaseaA.1.
ProDom	PDD000535; RNaseA.1.
SMART	SM00092; RNaseA_PC.1.
DR	PROSITE, PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW	Signal.
FT	SIGNAL. 1 22 POTENTIAL.
SQ	SEQUENCE 133 AA; 14615 MW; C8765B236B26E54E CRC64;

Query Match	48.7%	Score	281	DB	13	Length	133
Best Local Similarity	47.3%	Pred.	No.	1.7e-24			
Matches	52	Conservative	17	Mismatches	33	Indels	8
						Gaps	3

[illegible]

RESULT 11	
Q98SL8	
ID	PRELIMINARY;
Q98SL8	
00000000	PRT; 133 AA

DP 01-JUN-2001 (TREMBLrel_17, Created)
DT 01-JUN-2001 (TREMBLrel_17, Last sequence update)
DT 01-BEC-2001 (TREMBLrel_19, last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana
NCBI_TaxId=8400;
RN [1]
PP SEQUENCE FROM N.A.

ID	Q9DF78	PRELIMINARY;	PRT;	132 AA.
AC	Q9DF78;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	RC-RNaseL1 ribonuclease precursor.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_Taxid=8400;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=20512555; PubMed=11058105;			
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RT	"Purification and cloning of a cytosolic ribonucleases from Rana			
RL	catesbeiana (bullfrog).";			
RL	Nucleic Acids Res. 28:4097-4104(2000).			
LN	121			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RL	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;			
RL	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF288642; AAC30414.2;			
DR	HSSP: P11916; IBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF000074; rnaasea.1.			
DR	ProDom: PD000535; RNaseA.1.			
DR	SMART: SM00092; RNase_PC.1.			
DR	PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN.1.			
KW	Signal.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	132	RC-RNASEL1 RIBONUCLEASE.
SO	SEQUENCE	132 AA;	14625 MW;	D8D9A517452FBE53 CRC64;
QY	Query Match		46.98;	Score 270.5; DB 13; Length 132;
	Best Local Similarity		43.6%;	Pred. No. 2,7e-23;
	Matches	48;	Conservative	19; Mismatches 36; Indels 7; Gaps
Db	2 DMLFOKKHLITNRDVCNNINISNLF---HCKDKNTFYISRPPEYKAIICKIISKNV 57			
	23 NMAKFKKHLHTSISSIDCNTIMOKAIITYGCKKERNTFTIISSEDNVKAICSGVSPDKE 82			
QY	58 LTTSEFYLSDC---NVTSPCKYKLYKSTNTPFCVTCENQAPVHFVGVGH 104			
Db	83 LSTTSFKLNTCIRDSITPRPCPYHPSPDNKKICVKCEKQLPVHFGIGKC 132			
RESULT 14				
ID	Q9W738	PRELIMINARY;	PRT;	169 AA.
AC	Q9W738;			
DT	01-NOV-1999 (TrEMBLrel. 12, Created)			
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	FR12 protein.			
GN	FR12.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_Taxid=8355;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96069863; PubMed=7585965;			
RA	Kinoshita N., Minshull J., Kirschner M.W.;			
RT	"The identification of two novel ligands of the EGF receptor by a			
RL	yeast screening method and their activity in Xenopus development.";			
RL	Cell 83:621-630(1995).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RA	Kinoshita N., Kirschner M.W.;			

RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF159166; AAD41901.1; -
DR HSSP: P00656; 1LSO.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
SQ SEQUENCE 169 AA: 18851 MW: D969F3E43B3CE1B8 CRC64;

Query Match 27.3%; Score 157.5; DB 13; Length 169;
Best Local Similarity 36.1%; Pred. No. 2.9e-10;
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;

OY 6 FQKHLLNT-RDVDCN-----NIMSTNLFHCKDKDNFTFY-SRPEVKAICKGIASKNV 57
DB 33 FMEKHIVKGEAETNCNQTIKDNRIRFN--NCKFRNFTHDNTGKRYKEMCAGIYKSTFV 90
OY 58 LTTSEFYISDCNV---TSRP--CKYKLLKSTNTFCVTCENQAPVHVG 100
DB 91 ISKELLPLTDLCLMGRTARPNCAYNOTRTTGVINITCENNYPVHFAG 138

RESULT 15

O9UK15 PRELIMINARY; PRT; 152 AA.
AC O9UK15
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Eosinophil-associated ribonuclease 10.
GN EARI0.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20243759; Pubmed-10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection."
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL: AF238398; AAF67698.1; -
DR HSSP: P00656; 1LSO.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
SQ SEQUENCE 152 AA: 16830 MW: 780421C3661732C8 CRC64;

Query Match 23.1%; Score 133; DB 11; Length 152;
Best Local Similarity 30.3%; Pred. No. 1.7e-07;
Matches 37; Conservative 19; Mismatches 42; Indels 24; Gaps 6;

OY 1 SDMLTFQKKHLTNRDVCCNNIM--STNLFHCKDKDNFTFYSRPEVKAIC--KGIYA- 53
DB 31 SQM--FATQHTTNPANPCQNVEMLPINRNRTCKNINTELFHFNANVGVCGNPSGLCSN 88
OY 54 --SKNVLTSEFYISDCNVTSR-----PCKYKLLKSTNTFCVTCENQAP-----VHF 98
DB 89 NISTNCNNSRVPITVCNITSREKSCYOCRYOTRGSVGYTVACNPRTPQDSRPVYVHL 148
OY 99 VG 100
DB 149 DG 150

Search completed: June 25, 2003, 14:55:17
Job time : 26.4787 secs